GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 14:59:56 ; Search time 161.69 Seconds
(without alignments)
46.600 Million cell updates/sec

Title: US-08-887-505-47
Perfect score: 12
Sequence: 1 GGGGUCCUGGAG 12

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0601:*
1: /SIDS8/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqn/NA1982.DAT:*
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14: /SIDS8/gcgdata/geneseq/geneseqn/NA1993.DAT:*
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21: /SIDS8/gcgdata/geneseq/geneseqn/NA2000.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseqn/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | | 12 | 100.0 | 12 | 18 | AAT80257 | Oligo HCV82 used i |
| 2 | c | 12 | 100.0 | 12 | 20 | AAZ23540 | HCV wild type geno |
| 3 | c | 12 | 100.0 | 12 | 20 | AAX24037 | Ruthenium-labelled |
| 4 | c | 12 | 100.0 | 14 | 15 | AAQ70177 | Hepatitis C virus |
| 5 | | 12 | 100.0 | 15 | 15 | AAQ65140 | Antisense oligonuc |
| 6 | | 12 | 100.0 | 16 | 15 | AAQ65141 | Antisense oligonuc |
| 7 | | 12 | 100.0 | 16 | 15 | AAQ65125 | Antisense oligonuc |
| 8 | | 12 | 100.0 | 16 | 18 | AAT90622 | Hepatitis C virus |
| 9 | | 12 | 100.0 | 16 | 21 | AAA13439 | Hepatitis C virus |
| 10 | | 12 | 100.0 | 17 | 15 | AAQ65142 | Antisense oligonuc |
| 11 | | 12 | 100.0 | 17 | 15 | AAQ65126 | Antisense oligonuc |
| 12 | | 12 | 100.0 | 17 | 15 | AAQ65111 | Antisense oligonuc |
| 13 | | 12 | 100.0 | 18 | 15 | AAQ65143 | Antisense oligonuc |
| 14 | | 12 | 100.0 | 18 | 15 | AAQ65127 | Antisense oligonuc |
| 15 | | 12 | 100.0 | 18 | 15 | AAQ65112 | Antisense oligonuc |
| 16 | | 12 | 100.0 | 18 | 15 | AAQ65098 | Antisense oligonuc |
| 17 | | 12 | 100.0 | 18 | 18 | AAT80354 | Oligo HCV-209, tar |
| 18 | | 12 | 100.0 | 18 | 18 | AAT80355 | Oligo HCV-213, tar |
| 19 | | 12 | 100.0 | 18 | 18 | AAT80356 | Oligo HCV-216, tar |
| 20 | | 12 | 100.0 | 18 | 18 | AAT80357 | Oligo HCV-219, tar |
| 21 | | 12 | 100.0 | 18 | 18 | AAT80351 | Oligo HCV-197, tar |
| 22 | | 12 | 100.0 | 18 | 18 | AAT80352 | Oligo HCV-201, tar |
| 23 | | 12 | 100.0 | 18 | 18 | AAT80353 | Oligo HCV-205, tar |
| 24 | | 12 | 100.0 | 18 | 18 | AAT80259 | Oligo HCV90, targe |
| 25 | | 12 | 100.0 | 18 | 18 | AAT80260 | Oligo HCV91, targe |
| 26 | | 12 | 100.0 | 18 | 18 | AAT80261 | Oligo HCV93, targe |
| 27 | | 12 | 100.0 | 18 | 18 | AAT80262 | Oligo HCV94, targe |
| 28 | | 12 | 100.0 | 18 | 18 | AAT80263 | Oligo HCV96, targe |
| 29 | | 12 | 100.0 | 18 | 18 | AAT80264 | Oligo HCV97, targe |
| 30 | | 12 | 100.0 | 18 | 18 | AAT80248 | Oligo HCV94 used i |
| 31 | | 12 | 100.0 | 18 | 18 | AAT80249 | Oligo HCV53, targe |
| 32 | | 12 | 100.0 | 18 | 18 | AAT80250 | Oligo HCV54, targe |
| 33 | | 12 | 100.0 | 18 | 18 | AAT80251 | Oligo HCV55, targe |
| 34 | | 12 | 100.0 | 18 | 18 | AAT80252 | Oligo HCV56, targe |
| 35 | | 12 | 100.0 | 18 | 18 | AAT80253 | Oligo HCV59, targe |
| 36 | | 12 | 100.0 | 18 | 18 | AAT80254 | Oligo HCV60, targe |
| 37 | | 12 | 100.0 | 18 | 18 | AAT80255 | Oligo HCV61, targe |
| 38 | | 12 | 100.0 | 18 | 18 | AAT80256 | Oligo HCV62, targe |
| 39 | | 12 | 100.0 | 19 | 15 | AAQ65144 | Antisense oligonuc |
| 40 | | 12 | 100.0 | 19 | 15 | AAQ65128 | Antisense oligonuc |
| 41 | | 12 | 100.0 | 19 | 15 | AAQ65113 | Antisense oligonuc |
| 42 | | 12 | 100.0 | 19 | 15 | AAQ65086 | Antisense oligonuc |
| 43 | | 12 | 100.0 | 19 | 15 | AAQ65099 | Antisense oligonuc |
| 44 | | 12 | 100.0 | 19 | 15 | AAQ65100 | Antisense oligonuc |
| 45 | | 12 | 100.0 | 19 | 21 | AAZ99225 | Primer for primer- |

ALIGNMENTS

RESULT 1
AAT80257
ID AAT80257 standard; DNA; 12 BP.
XX
AC AAT80257;
XX
DT 15-OCT-1997 (first entry)
XX
DE Oligo HCV82 used in luciferase assay.
XX
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;
KW inhibition; replication; expression; detection; chronic hepatitis;
KW acute hepatitis; hepatocarcinoma; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..6
FT /*tag= a
FT /note= "Optionally 2'OMe modified"
FT modified_base 7..12
FT /*tag= b
FT /note= "Optionally comprises phosphorothioate linkages"
XX
PN WO9639500-A2.
XX
PD 12-DEC-1996.
XX
PF 04-JUN-1996; 96WO-EP02427.
XX
PR 06-JUN-1995; 95US-0471968.
XX
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA (HYBR-) HYBRIDON INC.

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XX
PI   Frank BL,  Goodchild J,  Hamlin HA,  Kilkuskie RE;
PI   Roberts NA,  Roberts PC, Walther DM,  Wolfe JL;
XX
DR   WPI; 1997-043122/04.
XX
PT   Oligo:nucleotide(s) complementary to HCV 5' untranslated region -
PT   used in the treatment and detection of HCV infection, esp. hepatitis
PT   and hepato-carcinoma
XX
PS   Claim 1; Page 31; 100pp; English.
XX
CC   The sequences given in AAT80211-382 represent synthetic oligonucleotides
CC   which are complementary to a portion of the 5' untranslated region (UTR)
CC   of hepatitis C virus (HCV).  These sequences may be used in a
CC   pharmaceutical composition for the control or prevention of HCV
CC   infection. They may be used to inhibit replication or expression of
CC   HCV or for detecting the presence of HCV in a sample.  They may be used
CC   to inhibit HCV replication in a cell and are therefor useful in the
CC   treatment of HCV infections such as chronic and acute hepatitis and
CC   hepatocarcinoma.  This oligo was used in a luciferase assay to determine
CC   whether it binds sucessfully to its target.
XX
SQ   Sequence 12 BP; 1 A; 2 C; 7 G; 2 U; 0 other;


  Query Match             100.0%;  Score 12;  DB 18;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||||||||||
Db      1 gggguccuggag 12


RESULT   2
AAZ23540/c
ID   AAZ23540 standard; DNA; 12 BP.
XX
AC   AAZ23540;
XX
DT   21-DEC-1999  (first entry)
XX
DE   HCV wild type genome probe.
XX
KW   Assay; amplification; hybridisation; probe; detection; viral; bacterial;
KW   cellular; yeast; fungal; primer; ss.
XX
OS   Synthetic.
OS   Hepatitis C virus.
XX
PN   DE19814828-A1.
XX
PD   07-OCT-1999.
XX
PF   02-APR-1998;   98DE-1014828.
XX
PR   02-APR-1998;   98DE-1014828.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
PI   Kessler C,  Haberhausen G,  Batz H,  Oerum H;
XX
DR   WPI; 1999-552286/47.
XX
PT   Nucleic acid amplification assay for detecting viral, bacterial,
PT   cellular, yeast or fungal nucleic acids  -
XX
PS   Example 1; Page 21; 28pp; German.
XX
CC   This invention describes a novel assay for a nucleic acid comprises:
CC   (a) generating amplification products from a fragment of the nucleic
CC   acid, (b) contacting the amplification products with a probe; and
CC   (c) detecting hybridization between the amplification product and the
CC   probe. The assay is useful for detection of viral, bacterial, cellular,
CC   yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
CC   or fungal samples, e.g. feces, smears, cell suspensions, cultures or
CC   tissue, cell or liquid biopsy samples. This sequence represents a
CC   probe used in the method of the invention.
XX
SQ   Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 other;


  Query Match             100.0%;  Score 12;  DB 20;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db     12 GGGGTCCTGGAG 1


RESULT   3
AAX24037/c
ID   AAX24037 standard; DNA; 12 BP.
XX
AC   AAX24037;
XX
DT   28-JUN-1999  (first entry)
XX
DE   Ruthenium-labelled DNA probe.
XX
KW   Amplification; medical; forensic; diagnosis; food analysis; blood;
KW   environmental analysis; plant protection; veterinary medicine;
KW   human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia;
KW   screening; PCR primer; detection; probe; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /note= "5'-end labelled with ruthenium""
XX
PN   DE19748690-A1.
XX
PD   06-MAY-1999.
XX
PF   04-NOV-1997;   97DE-1048690.
XX
PR   04-NOV-1997;   97DE-1048690.
XX
PA   (HOFF ) ROCHE DIAGNOSTICS GMBH.
XX
DR   WPI; 1999-278780/24.
XX
PT   Detecting nucleic acid by generating short amplicons and probing
PT   e.g. for diagnosis, food and environmental analysis and plant
PT   protection
XX
PS   Example 1; Page 18; 22pp; German.
XX
CC   This invention describes a method for the detection of nucleic acid
CC   which comprises amplification and reaction of the amplicon with a probe.
CC   The method is used to detect nucleic acid e.g. for medical or forensic
CC   diagnosis, in food and environmental analysis, in plant protection and
CC   veterinary medicine, e.g. for detecting human immune deficiency virus,
CC   hepatitis B or C viruses, or Chlamydia, in blood screening. The method
CC   provides target-dependent, exponential amplification for highly specific
CC   and sensitive, reproducible and quantitative detection of one or more
CC   nucleic acids (single or double stranded). The design of primers and
CC   probes is sufficiently flexible to allow many nucleic acids to be
CC   detected in a standardized reaction format using partly the same primers
CC   and probes. Only small amplicons are produced (requiring short
CC   amplification cycles), there is no competition/displacement between the
CC   short counter-strand of the amplicon and the detection probe, and
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CC   specificity is high because the relative proportion of the internal
CC   detection region is increased with respect to the total amplicon length,
CC   allowing better differentiation between (viral) subtypes. Also short
CC   amplicons are less likely to undergo non-specific hybridization, so
CC   background is low, and short RNA sequences are more stable, with reduced
CC   tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
CC   PCR primers and probes used in the method of the invention.
XX
SQ   Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 other;


  Query Match            100.0%;  Score 12;  DB 20;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db     12 GGGGTCCTGGAG 1


RESULT   4
AAQ70177/c
ID   AAQ70177 standard; RNA; 14 BP.
XX
AC   AAQ70177;
XX
DT   04-OCT-1994  (first entry)
XX
DE   Hepatitis C virus 5'-UTR antisense oligonucleotide target (A).
XX
KW   Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
KW   antisense oligonucleotide; translation inhibition; therapy;
KW   5'-untranslated region; ss.
XX
OS   Hepatitis C Virus.
XX
PN   WO9405813-A.
XX
PD   17-MAR-1994.
XX
PF   10-SEP-1993;   93WO-JP01293.
XX
PR   10-SEP-1992;   92US-0945289.
PR   14-APR-1993;   93JP-0087195.
XX
PA   (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PA   (ISIS-) ISIS PHARM INC.
PA   (MOCH ) MOCHIDA PHARM CO LTD.
XX
PI   Anderson KP,  Eto T,  Furukawa S,  Hamada F,  Hanecak RC;
PI   Hoshiko K,  Nakatake H,  Nishihara T,  Nozaki C;
XX
DR   WPI; 1994-101217/12.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral
PT   genome - useful for inhibiting HCV replication, to treat related
PT   diseases
XX
PS   Claim 16; Page 71; 91pp; English.
XX
CC   Oligonucleotides which are complementary to part of the hepatitis
CC   C virus genomic or messenger RNA are claimed. AAQ70177 is a preferred
CC   target sequence which is present in the 5'-UTR of the HCV genome.
XX
SQ   Sequence 14 BP; 2 A; 8 C; 3 G; 1 U; 0 other;


  Query Match            100.0%;  Score 12;  DB 15;  Length 14;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db     14 GGGGTCCTGGAG 3


RESULT   5
AAQ65140
ID   AAQ65140 standard; DNA; 15 BP.
XX
AC   AAQ65140;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 163; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 15 BP; 1 A; 2 C; 10 G; 2 T; 0 other;


  Query Match            100.0%;  Score 12;  DB 15;  Length 15;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db      4 ggggtcctggag 15


RESULT   6
AAQ65141
ID   AAQ65141 standard; DNA; 16 BP.
XX
AC   AAQ65141;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
```

```
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 163; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 16 BP; 2 A; 2 C; 10 G; 2 T; 0 other;


  Query Match            100.0%;  Score 12;  DB 15;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGGUCCUGGAG 12
           ||||:||:||||
Db       5 ggggtcctggag 16


RESULT   7
AAQ65125
ID   AAQ65125 standard; DNA; 16 BP.
XX
AC   AAQ65125;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 156; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 16 BP; 1 A; 2 C; 11 G; 2 T; 0 other;


  Query Match            100.0%;  Score 12;  DB 15;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGGUCCUGGAG 12
           ||||:||:||||
Db       4 ggggtcctggag 15


RESULT   8
AAT90622
ID   AAT90622 standard; RNA; 16 BP.
XX
AC   AAT90622;
XX
DT   07-APR-1998  (first entry)
XX
DE   Hepatitis C virus recognition sequence 32 for ribozyme cleavage.
XX
KW   Recognition sequence; HCV; ribozyme; 5' untranslated region;
KW   nucleocapsid coding region; hairpin ribozyme; RNA cleavage;
KW   treatment; HCV infection; HCV contamination; ss.
XX
OS   Hepatitis C virus.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    1..4
FT                   /*tag=  a
FT                   /note= "complementary to the CNR2 ribozyme"
FT   misc_feature    6
FT                   /*tag=  b
FT                   /note= "cleavage site corresponding to position 120
FT                          of the (-) strand, counting from 3' end"
FT   misc_feature    9..16
FT                   /*tag=  c
FT                   /note= "complementary to the CNR2 ribozyme"
XX
PN   WO9732018-A2.
XX
PD   04-SEP-1997.
XX
PF   27-FEB-1997;   97WO-US03304.
XX
PR   29-FEB-1996;   96US-0608862.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Barber JR,  Tritz R,  Welch PJ,  Yei S,  Yu M;
XX
DR   WPI; 1997-470461/43.
XX
PT   Ribozyme(s) directed against hepatitis C virus - for prevention and
PT   treatment of viral infection, and detection of HCV contamination of
PT   blood
XX
PS   Example 1; Page 17; 98pp; English.
XX
CC   AAT90621-650 represent recognition sequences found in the positive (-)
CC   strand of the Hepatitis C virus (HCV) RNA. The sequences are recognised
CC   by novel ribozymes which inhibit replication, infectivity or gene
CC   expression of HCV. The present sequence is located within the 5' UTR.
CC   Hairpin ribozymes of the present invention were designed based on
CC   sequences adjacent to the GUC sequence recognition feature. The
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CC   ribozymes are directed against conserved regions of the genome and so
CC   should be active against many strains of HCV. The ribozymes, when
CC   optionally expressed from a vector, cleave the RNA of HCV and so are
CC   useful for treatment and prevention of HCV infection. They can also be
CC   used to detect HCV contamination of blood or for clinical diagnosis.
XX
SQ   Sequence 16 BP; 1 A; 3 C; 10 G; 2 U; 0 other;


  Query Match             100.0%;  Score 12;  DB 18;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||||||||||
Db      3 gggguccuggag 14


RESULT  9
AAA13439
ID   AAA13439 standard; RNA; 16 BP.
XX
AC   AAA13439;
XX
DT   17-JUL-2000  (first entry)
XX
DE   Hepatitis C virus hairpin ribozyme recognition sequence SEQ ID NO:39.
XX
KW   Hepatitis C virus; HCV; hairpin ribozyme; cleavage; recognition site;
KW   infection; virucide; hepatotropic; antiinflammatory;
KW   replication inhibitor; gene expression inhibitor; ss.
XX
OS   Hepatitis C virus.
XX
PN   US6043077-A.
XX
PD   28-MAR-2000.
XX
PF   20-OCT-1997;   97US-0954210.
XX
PR   29-FEB-1996;   97US-0608862.
PR   27-FEB-1997;   97WO-US03304.
XX
PA   (IMMU-) IMMUSOL INC.
XX
PI   Tritz R,  Yei S,  Yu M,  Barber JR,  Welch PJ;
XX
DR   WPI; 2000-270342/23.
XX
PT   Ribozyme capable of inhibiting replication, infectivity or gene
PT   expression of hepatitis C virus, useful for treating or preventing
PT   hepatitis C virus infection  -
XX
PS   Claim 1; Column 13; 57pp; English.
XX
CC   The present invention describes ribozymes (I) capable of inhibiting
CC   replication, infectivity or gene expression of a hepatitis C virus
CC   (HCV), directed to target sequences AAA13438 to AAA13444, AAA13454 and
CC   AAA13465. (I) have virucide, hepatotropic and antiinflammatory
CC   activities. (I), or vectors comprising nucleotide sequences encoding (I),
CC   are useful for interfering with the replication or gene expression of HCV
CC   in a human cells. (I) are useful for diagnosis, prevention and treatment
CC   of HCV infection or disease in a mammals especially humans. Nucleotide
CC   sequences encoding (I) are useful for preventing hepatitis C viral
CC   infection in a cell. AAA13401 to AAA13405 represent examples of the
CC   briefest requirements for hairpin ribozyme; AAA13406 and AAA13407
CC   represent PCR primers used in the amplification of the HCV capsid
CC   sequence; AAA13408 to AAA13467 represent HCV hairpin ribozyme recognition
CC   sites; and AAA13468 to AAA13473 represent oligonucleotides used in the
CC   construction of HCV hairpin ribozymes, all these sequences are used in
CC   the exemplification of the present invention.
XX
SQ   Sequence 16 BP; 1 A; 3 C; 10 G; 2 U; 0 other;


  Query Match             100.0%;  Score 12;  DB 21;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 1e+03;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||||||||||
Db      3 gggguccuggag 14


RESULT  10
AAQ65142
ID   AAQ65142 standard; DNA; 17 BP.
XX
AC   AAQ65142;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 164; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 other;


  Query Match             100.0%;  Score 12;  DB 15;  Length 17;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db      6 ggggtcctggag 17


RESULT  11
AAQ65126
ID   AAQ65126 standard; DNA; 17 BP.
XX
AC   AAQ65126;
XX
DT   21-DEC-1994  (first entry)
XX
```

```
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 157; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 17 BP; 2 A; 2 C; 11 G; 2 T; 0 other;


  Query Match             100.0%;  Score 12;  DB 15;  Length 17;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGGUCCUGGAG 12
           ||||:||:||||
Db       5 ggggtcctggag 16


RESULT  12
AAQ65111
ID   AAQ65111 standard; DNA; 17 BP.
XX
AC   AAQ65111;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 150; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 17 BP; 1 A; 3 C; 11 G; 2 T; 0 other;


  Query Match             100.0%;  Score 12;  DB 15;  Length 17;
  Best Local Similarity   83.3%;  Pred. No. 1e+03;
  Matches   10;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 GGGGUCCUGGAG 12
           ||||:||:||||
Db       4 ggggtcctggag 15


RESULT  13
AAQ65143
ID   AAQ65143 standard; DNA; 18 BP.
XX
AC   AAQ65143;
XX
DT   21-DEC-1994  (first entry)
XX
DE   Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW   Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW   therapy; inhibition; viral protein precursor; ss.
XX
OS   Synthetic.
XX
PN   CA2104649-A.
XX
PD   26-FEB-1994.
XX
PF   23-AUG-1993;   93CA-2104649.
XX
PR   25-AUG-1992;   92JP-0248796.
PR   03-MAR-1993;   93JP-0042736.
XX
PA   (SEKI/) SEKI M.
XX
PI   Honda Y,  Seki M,  Yamada E;
XX
DR   WPI; 1994-151836/19.
XX
PT   Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT   virus genome - are useful as antiviral agents
XX
PS   Claim 5; Page 164; 262pp; English.
XX
CC   This oligonucleotide is an example of a preferred antisense compound
CC   i.e. it has a base sequence of 15-30 bases which is included
CC   within the 49 bases from G at position 127 to C at position 175 of
CC   AAQ64913 and which contains at least 7 bases from C at position 147
CC   to C at position 153. The antisense oligonucleotide is useful for
CC   inhibiting translation of HCV genes.
XX
SQ   Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 other;


  Query Match             100.0%;  Score 12;  DB 15;  Length 18;
```

Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db      7 ggggtcctggag 18
```

RESULT 14
AAQ65127
ID AAQ65127 standard; DNA; 18 BP.
XX
AC AAQ65127;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 157; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 18 BP; 2 A; 2 C; 12 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db      6 ggggtcctggag 17
```

RESULT 15
AAQ65112
ID AAQ65112 standard; DNA; 18 BP.
XX
AC AAQ65112;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 151; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 18 BP; 2 A; 3 C; 11 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 GGGGUCCUGGAG 12
          ||||:||:||||
Db      5 ggggtcctggag 16
```

Search completed: August 8, 2001, 16:06:02
Job time: 3966 sec

GenCore version 4.5


OM nucleic - nucleic search, using sw model

Run on: August 8, 2001, 16:01:27 ; Search time 1583.8 Seconds
(without alignments)
195.325 Million cell updates/sec

Title: US-08-887-505-122
Perfect score: 20
Sequence: 1 UUCGCGACCCAACACUACUC 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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97: gb_pr10:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| c | 1 | 20 | 100.0 | 27 | 9 | AR106359 | AR106359 Sequence |
| | 2 | 20 | 100.0 | 33 | 9 | AR004396 | AR004396 Sequence |
| | 3 | 20 | 100.0 | 33 | 9 | AR064935 | AR064935 Sequence |
| | 4 | 20 | 100.0 | 33 | 9 | AR097188 | AR097188 Sequence |
| | 5 | 20 | 100.0 | 33 | 10 | I82871 | I82871 Sequence 50 |
| | 6 | 20 | 100.0 | 46 | 10 | I44581 | I44581 Sequence 10 |
| | 7 | 20 | 100.0 | 46 | 10 | I70986 | I70986 Sequence 10 |
| c | 8 | 20 | 100.0 | 139 | 58 | AF282631 | AF282631 Hepatitis |

| | | | | | | |
|---|---|---|---|---|---|---|
| c 9 | 20 | 100.0 | 139 | 58 | AF282632 | AF282632 Hepatitis |
| c 10 | 20 | 100.0 | 139 | 58 | AF282633 | AF282633 Hepatitis |
| c 11 | 20 | 100.0 | 139 | 58 | AF282634 | AF282634 Hepatitis |
| c 12 | 20 | 100.0 | 139 | 58 | AF282635 | AF282635 Hepatitis |
| c 13 | 20 | 100.0 | 139 | 58 | AF282637 | AF282637 Hepatitis |
| c 14 | 20 | 100.0 | 139 | 58 | AF282638 | AF282638 Hepatitis |
| c 15 | 20 | 100.0 | 139 | 58 | AF282639 | AF282639 Hepatitis |
| c 16 | 20 | 100.0 | 139 | 58 | AF282640 | AF282640 Hepatitis |
| c 17 | 20 | 100.0 | 139 | 58 | AF282641 | AF282641 Hepatitis |
| c 18 | 20 | 100.0 | 139 | 58 | AF282642 | AF282642 Hepatitis |
| c 19 | 20 | 100.0 | 139 | 58 | AF282643 | AF282643 Hepatitis |
| c 20 | 20 | 100.0 | 139 | 58 | AF282644 | AF282644 Hepatitis |
| c 21 | 20 | 100.0 | 139 | 58 | AF282645 | AF282645 Hepatitis |
| c 22 | 20 | 100.0 | 139 | 58 | AF282646 | AF282646 Hepatitis |
| c 23 | 20 | 100.0 | 139 | 58 | AY003921 | AY003921 Hepatitis |
| c 24 | 20 | 100.0 | 139 | 58 | AY003922 | AY003922 Hepatitis |
| c 25 | 20 | 100.0 | 139 | 58 | AY003923 | AY003923 Hepatitis |
| c 26 | 20 | 100.0 | 139 | 58 | AY003924 | AY003924 Hepatitis |
| c 27 | 20 | 100.0 | 139 | 58 | AY003925 | AY003925 Hepatitis |
| c 28 | 20 | 100.0 | 139 | 58 | AY003928 | AY003928 Hepatitis |
| c 29 | 20 | 100.0 | 139 | 58 | AY003929 | AY003929 Hepatitis |
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| c 31 | 20 | 100.0 | 139 | 58 | AY003932 | AY003932 Hepatitis |
| c 32 | 20 | 100.0 | 139 | 58 | AY003933 | AY003933 Hepatitis |
| c 33 | 20 | 100.0 | 139 | 58 | AY003934 | AY003934 Hepatitis |
| c 34 | 20 | 100.0 | 139 | 58 | AY003935 | AY003935 Hepatitis |
| c 35 | 20 | 100.0 | 139 | 58 | AY003936 | AY003936 Hepatitis |
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| c 37 | 20 | 100.0 | 139 | 58 | AY003938 | AY003938 Hepatitis |
| c 38 | 20 | 100.0 | 139 | 58 | AY003939 | AY003939 Hepatitis |
| c 39 | 20 | 100.0 | 139 | 58 | AY003940 | AY003940 Hepatitis |
| c 40 | 20 | 100.0 | 139 | 58 | AY003941 | AY003941 Hepatitis |
| c 41 | 20 | 100.0 | 139 | 58 | AY003942 | AY003942 Hepatitis |
| c 42 | 20 | 100.0 | 139 | 58 | AY003943 | AY003943 Hepatitis |
| c 43 | 20 | 100.0 | 139 | 58 | AY003944 | AY003944 Hepatitis |
| c 44 | 20 | 100.0 | 139 | 58 | AY003945 | AY003945 Hepatitis |
| c 45 | 20 | 100.0 | 139 | 58 | AY004013 | AY004013 Hepatitis |

ALIGNMENTS

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RESULT   1
AR106359/c
LOCUS       AR106359       27 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 21 from patent US 6107028.
ACCESSION   AR106359
VERSION     AR106359.1  GI:12820889
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kay,M.A. and Lieber,A.
  TITLE     Ribozymes for treating hepatitis C
  JOURNAL   Patent: US 6107028-A 21 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        6 a      4 c     12 g      5 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 9;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db     24 TTCGCGACCCAACACTACTC 5


RESULT   2
AR004396
LOCUS       AR004396       33 bp    DNA             PAT       04-DEC-1998
DEFINITION  Sequence 50 from patent US 5747244.
ACCESSION   AR004396
VERSION     AR004396.1  GI:3965275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
  TITLE     Nucleic acid probes immobilized on polystyrene surfaces
  JOURNAL   Patent: US 5747244-A 50 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      13 c      6 g      6 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 9;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
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Db     10 TTCGCGACCCAACACTACTC 29


RESULT   3
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LOCUS       AR064935       33 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 60 from patent US 5849481.
ACCESSION   AR064935
VERSION     AR064935.1  GI:5995151
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Urdea,M.S., Horn,T., Chang,C., Warner,B. and Fultz,T.J.
  TITLE     Nucleic acid hybridization assays employing large comb-type
            branched polynucleotides
  JOURNAL   Patent: US 5849481-A 60 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      13 c      6 g      6 t
ORIGIN


  Query Match           100.0%;  Score 20;  DB 9;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db     10 TTCGCGACCCAACACTACTC 29


RESULT   4
AR097188
LOCUS       AR097188       33 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 126 from patent US 6071693.
ACCESSION   AR097188
VERSION     AR097188.1  GI:12805918
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cha,T., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
  TITLE     HCV genomic sequences for diagnostics and therapeutics
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  JOURNAL   Patent: US 6071693-A 126 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      13 c       6 g       6 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 9;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db     10 TTCGCGACCCAACACTACTC 29
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RESULT   5
I82871
LOCUS       I82871          33 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 50 from patent US 5712383.
ACCESSION   I82871
VERSION     I82871.1  GI:3211168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
  TITLE     Process for immobilizing nucleic acid probes on polystyrene
            surfaces
  JOURNAL   Patent: US 5712383-A 50 27-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a      13 c       6 g       6 t
ORIGIN
```

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  Query Match             100.0%;  Score 20;  DB 10;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db     10 TTCGCGACCCAACACTACTC 29
```

```
RESULT   6
I44581
LOCUS       I44581          46 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 10 from patent US 5635352.
ACCESSION   I44581
VERSION     I44581.1  GI:2469294
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise
  JOURNAL   Patent: US 5635352-A 10 03-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="unknown"
BASE COUNT        9 a      17 c      11 g       9 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 10;  Length 46;
  Best Local Similarity   80.0%;  Pred. No. 0.45;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db     10 TTCGCGACCCAACACTACTC 29
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```
RESULT   7
I70986
LOCUS       I70986          46 bp    DNA             PAT       03-APR-1998
DEFINITION  Sequence 10 from patent US 5681697.
ACCESSION   I70986
VERSION     I70986.1  GI:3007121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise and kits therefor
  JOURNAL   Patent: US 5681697-A 10 28-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="unknown"
BASE COUNT        9 a      17 c      11 g       9 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 10;  Length 46;
  Best Local Similarity   80.0%;  Pred. No. 0.45;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db     10 TTCGCGACCCAACACTACTC 29
```

```
RESULT   8
AF282631/c
LOCUS       AF282631        139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H069 clone I 5' non-coding region
            sequence.
ACCESSION   AF282631
VERSION     AF282631.1  GI:10764494
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H069"
                     /db_xref="taxon:11103"
                     /clone="I"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       28 a      36 c      43 g      32 t
ORIGIN
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Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db    116 TTCGCGACCCAACACTACTC 97


RESULT   9
AF282632/c
LOCUS       AF282632      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H069 clone II 5' non-coding region
            sequence.
ACCESSION   AF282632
VERSION     AF282632.1  GI:10764495
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H069"
                     /db_xref="taxon:11103"
                     /clone="II"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       28 a     36 c     42 g     33 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db    116 TTCGCGACCCAACACTACTC 97


RESULT  10
AF282633/c
LOCUS       AF282633      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H071 clone I 5' non-coding region
            sequence.
ACCESSION   AF282633
VERSION     AF282633.1  GI:10764496
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H071"
                     /db_xref="taxon:11103"
                     /clone="I"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       27 a     37 c     43 g     32 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db    116 TTCGCGACCCAACACTACTC 97


RESULT  11
AF282634/c
LOCUS       AF282634      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H071 clone II 5' non-coding region
            sequence.
ACCESSION   AF282634
VERSION     AF282634.1  GI:10764497
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H071"
                     /db_xref="taxon:11103"
                     /clone="II"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       27 a     38 c     43 g     31 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 UUCGCGACCCAACACUACUC 20
          ::|||||||||||||:||:|
Db    116 TTCGCGACCCAACACTACTC 97


RESULT  12
AF282635/c
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LOCUS       AF282635      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H075 clone I 5' non-coding region
            sequence.
ACCESSION   AF282635
VERSION     AF282635.1  GI:10764498
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H075"
                     /db_xref="taxon:11103"
                     /clone="I"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       26 a     37 c     44 g     32 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||:||:|
Db     116 TTCGCGACCCAACACTACTC 97


RESULT  13
AF282637/c
LOCUS       AF282637      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H075 clone III 5' non-coding region
            sequence.
ACCESSION   AF282637
VERSION     AF282637.1  GI:10764500
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H075"
                     /db_xref="taxon:11103"
                     /clone="III"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       26 a     36 c     44 g     33 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||:||:|
Db     116 TTCGCGACCCAACACTACTC 97


RESULT  14
AF282638/c
LOCUS       AF282638      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H075 clone IV 5' non-coding region
            sequence.
ACCESSION   AF282638
VERSION     AF282638.1  GI:10764501
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H075"
                     /db_xref="taxon:11103"
                     /clone="IV"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       26 a     36 c     44 g     33 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||:||:|
Db     116 TTCGCGACCCAACACTACTC 97


RESULT  15
AF282639/c
LOCUS       AF282639      139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H858 clone I 5' non-coding region
            sequence.
ACCESSION   AF282639
VERSION     AF282639.1  GI:10764502
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
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  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
                     /isolate="H858"
                     /db_xref="taxon:11103"
                     /clone="I"
     misc_feature    1. .139
                     /note="5' non-coding region"
BASE COUNT       26 a     37 c     44 g     32 t
ORIGIN


  Query Match             100.0%;  Score 20;  DB 58;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 0.46;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||:||:|
Db     116 TTCGCGACCCAACACTACTC 97


Search completed: August  8, 2001, 16:01:28
Job time: 5802 sec
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CC specificity is high because the relative proportion of the internal
CC detection region is increased with respect to the total amplicon length,
CC allowing better differentiation between (viral) subtypes. Also short
CC amplicons are less likely to undergo non-specific hybridization, so
CC background is low, and short RNA sequences are more stable, with reduced
CC tendency to form secondary structures. AAX23968-69 and AAX24035-37 are
CC PCR primers and probes used in the method of the invention.
XX
SQ Sequence 12 BP; 2 A; 7 C; 2 G; 1 T; 0 other;

Query Match 100.0%; Score 12; DB 20; Length 12;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGGAG 12
||||:||:||||
Db 12 GGGGTCCTGGAG 1

RESULT 4
AAQ70177/c
ID AAQ70177 standard; RNA; 14 BP.
XX
AC AAQ70177;
XX
DT 04-OCT-1994 (first entry)
XX
DE Hepatitis C virus 5'-UTR antisense oligonucleotide target (A).
XX
KW Hepatitis C virus; HCV; non-A, non-B hepatitis virus; NANBHV;
KW antisense oligonucleotide; translation inhibition; therapy;
KW 5'-untranslated region; ss.
XX
OS Hepatitis C Virus.
XX
PN WO9405813-A.
XX
PD 17-MAR-1994.
XX
PF 10-SEP-1993; 93WO-JP01293.
XX
PR 10-SEP-1992; 92US-0945289.
PR 14-APR-1993; 93JP-0087195.
XX
PA (KAGA ) CHEMO SERO THERAPEUTIC RES INST.
PA (ISIS-) ISIS PHARM INC.
PA (MOCH ) MOCHIDA PHARM CO LTD.
XX
PI Anderson KP, Eto T, Furukawa S, Hamada F, Hanecak RC;
PI Hoshiko K, Nakatake H, Nishihara T, Nozaki C;
XX
DR WPI; 1994-101217/12.
XX
PT Anti:sense oligo:nucleotide(s) complementary to hepatitis C viral
PT genome - useful for inhibiting HCV replication, to treat related
PT diseases
XX
PS Claim 16; Page 71; 91pp; English.
XX
CC Oligonucleotides which are complementary to part of the hepatitis
CC C virus genomic or messenger RNA are claimed. AAQ70177 is a preferred
CC target sequence which is present in the 5'-UTR of the HCV genome.
XX
SQ Sequence 14 BP; 2 A; 8 C; 3 G; 1 U; 0 other;

Query Match 100.0%; Score 12; DB 15; Length 14;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGGAG 12
||||:||:||||
Db 14 GGGGTCCTGGAG 3

RESULT 5
AAQ65140
ID AAQ65140 standard; DNA; 15 BP.
XX
AC AAQ65140;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
PT virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 163; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound
CC i.e. it has a base sequence of 15-30 bases which is included
CC within the 49 bases from G at position 127 to C at position 175 of
CC AAQ64913 and which contains at least 7 bases from C at position 147
CC to C at position 153. The antisense oligonucleotide is useful for
CC inhibiting translation of HCV genes.
XX
SQ Sequence 15 BP; 1 A; 2 C; 10 G; 2 T; 0 other;

Query Match 100.0%; Score 12; DB 15; Length 15;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGUCCUGGAG 12
||||:||:||||
Db 4 ggggtcctggag 15

RESULT 6
AAQ65141
ID AAQ65141 standard; DNA; 16 BP.
XX
AC AAQ65141;
XX
DT 21-DEC-1994 (first entry)
XX
DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
KW therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.

| | | | | | | |
|---|---|---|---|---|---|---|
| c 9 | 20 | 100.0 | 139 | 58 | AF282632 | AF282632 Hepatitis |
| c 10 | 20 | 100.0 | 139 | 58 | AF282633 | AF282633 Hepatitis |
| c 11 | 20 | 100.0 | 139 | 58 | AF282634 | AF282634 Hepatitis |
| c 12 | 20 | 100.0 | 139 | 58 | AF282635 | AF282635 Hepatitis |
| c 13 | 20 | 100.0 | 139 | 58 | AF282637 | AF282637 Hepatitis |
| c 14 | 20 | 100.0 | 139 | 58 | AF282638 | AF282638 Hepatitis |
| c 15 | 20 | 100.0 | 139 | 58 | AF282639 | AF282639 Hepatitis |
| c 16 | 20 | 100.0 | 139 | 58 | AF282640 | AF282640 Hepatitis |
| c 17 | 20 | 100.0 | 139 | 58 | AF282641 | AF282641 Hepatitis |
| c 18 | 20 | 100.0 | 139 | 58 | AF282642 | AF282642 Hepatitis |
| c 19 | 20 | 100.0 | 139 | 58 | AF282643 | AF282643 Hepatitis |
| c 20 | 20 | 100.0 | 139 | 58 | AF282644 | AF282644 Hepatitis |
| c 21 | 20 | 100.0 | 139 | 58 | AF282645 | AF282645 Hepatitis |
| c 22 | 20 | 100.0 | 139 | 58 | AF282646 | AF282646 Hepatitis |
| c 23 | 20 | 100.0 | 139 | 58 | AY003921 | AY003921 Hepatitis |
| c 24 | 20 | 100.0 | 139 | 58 | AY003922 | AY003922 Hepatitis |
| c 25 | 20 | 100.0 | 139 | 58 | AY003923 | AY003923 Hepatitis |
| c 26 | 20 | 100.0 | 139 | 58 | AY003924 | AY003924 Hepatitis |
| c 27 | 20 | 100.0 | 139 | 58 | AY003925 | AY003925 Hepatitis |
| c 28 | 20 | 100.0 | 139 | 58 | AY003928 | AY003928 Hepatitis |
| c 29 | 20 | 100.0 | 139 | 58 | AY003929 | AY003929 Hepatitis |
| c 30 | 20 | 100.0 | 139 | 58 | AY003930 | AY003930 Hepatitis |
| c 31 | 20 | 100.0 | 139 | 58 | AY003932 | AY003932 Hepatitis |
| c 32 | 20 | 100.0 | 139 | 58 | AY003933 | AY003933 Hepatitis |
| c 33 | 20 | 100.0 | 139 | 58 | AY003934 | AY003934 Hepatitis |
| c 34 | 20 | 100.0 | 139 | 58 | AY003935 | AY003935 Hepatitis |
| c 35 | 20 | 100.0 | 139 | 58 | AY003936 | AY003936 Hepatitis |
| c 36 | 20 | 100.0 | 139 | 58 | AY003937 | AY003937 Hepatitis |
| c 37 | 20 | 100.0 | 139 | 58 | AY003938 | AY003938 Hepatitis |
| c 38 | 20 | 100.0 | 139 | 58 | AY003939 | AY003939 Hepatitis |
| c 39 | 20 | 100.0 | 139 | 58 | AY003940 | AY003940 Hepatitis |
| c 40 | 20 | 100.0 | 139 | 58 | AY003941 | AY003941 Hepatitis |
| c 41 | 20 | 100.0 | 139 | 58 | AY003942 | AY003942 Hepatitis |
| c 42 | 20 | 100.0 | 139 | 58 | AY003943 | AY003943 Hepatitis |
| c 43 | 20 | 100.0 | 139 | 58 | AY003944 | AY003944 Hepatitis |
| c 44 | 20 | 100.0 | 139 | 58 | AY003945 | AY003945 Hepatitis |
| c 45 | 20 | 100.0 | 139 | 58 | AY004013 | AY004013 Hepatitis |

ALIGNMENTS

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RESULT   1
AR106359/c
LOCUS       AR106359       27 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 21 from patent US 6107028.
ACCESSION   AR106359
VERSION     AR106359.1  GI:12820889
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Kay,M.A. and Lieber,A.
  TITLE     Ribozymes for treating hepatitis C
  JOURNAL   Patent: US 6107028-A 21 22-AUG-2000;
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="unknown"
BASE COUNT        6 a      4 c     12 g      5 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 9;  Length 27;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||:||:|
Db      24 TTCGCGACCCAACACTACTC 5
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AR004396
LOCUS       AR004396       33 bp    DNA             PAT       04-DEC-1998
DEFINITION  Sequence 50 from patent US 5747244.
ACCESSION   AR004396
VERSION     AR004396.1  GI:3965275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
  TITLE     Nucleic acid probes immobilized on polystyrene surfaces
  JOURNAL   Patent: US 5747244-A 50 05-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .33
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BASE COUNT        8 a      13 c      6 g      6 t
ORIGIN


  Query Match            100.0%;  Score 20;  DB 9;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
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Db      10 TTCGCGACCCAACACTACTC 29


RESULT   3
AR064935
LOCUS       AR064935       33 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 60 from patent US 5849481.
ACCESSION   AR064935
VERSION     AR064935.1  GI:5995151
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Urdea,M.S., Horn,T., Chang,C., Warner,B. and Fultz,T.J.
  TITLE     Nucleic acid hybridization assays employing large comb-type
            branched polynucleotides
  JOURNAL   Patent: US 5849481-A 60 15-DEC-1998;
FEATURES             Location/Qualifiers
     source          1. .33
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BASE COUNT        8 a      13 c      6 g      6 t
ORIGIN


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  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||:||:|
Db      10 TTCGCGACCCAACACTACTC 29


RESULT   4
AR097188
LOCUS       AR097188       33 bp    DNA             PAT       14-FEB-2001
DEFINITION  Sequence 126 from patent US 6071693.
ACCESSION   AR097188
VERSION     AR097188.1  GI:12805918
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Cha,T., Beall,E., Irvine,B., Kolberg,J. and Urdea,M.S.
  TITLE     HCV genomic sequences for diagnostics and therapeutics
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  JOURNAL   Patent: US 6071693-A 126 06-JUN-2000;
FEATURES             Location/Qualifiers
     source          1. .33
                     /organism="unknown"
BASE COUNT        8 a     13 c      6 g      6 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 9;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||||:||:|
Db      10 TTCGCGACCCAACACTACTC 29
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RESULT   5
I82871
LOCUS       I82871         33 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 50 from patent US 5712383.
ACCESSION   I82871
VERSION     I82871.1  GI:3211168
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 33)
  AUTHORS   Sheridan,P., Chang,C., Running,J. and Urdea,M.S.
  TITLE     Process for immobilizing nucleic acid probes on polystyrene
            surfaces
  JOURNAL   Patent: US 5712383-A 50 27-JAN-1998;
FEATURES             Location/Qualifiers
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                     /organism="unknown"
BASE COUNT        8 a     13 c      6 g      6 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 10;  Length 33;
  Best Local Similarity   80.0%;  Pred. No. 0.44;
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Qy       1 UUCGCGACCCAACACUACUC 20
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Db      10 TTCGCGACCCAACACTACTC 29
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RESULT   6
I44581
LOCUS       I44581         46 bp    DNA             PAT       07-OCT-1997
DEFINITION  Sequence 10 from patent US 5635352.
ACCESSION   I44581
VERSION     I44581.1  GI:2469294
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise
  JOURNAL   Patent: US 5635352-A 10 03-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="unknown"
BASE COUNT        9 a     17 c      11 g      9 t
ORIGIN
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  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
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Db      10 TTCGCGACCCAACACTACTC 29
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RESULT   7
I70986
LOCUS       I70986         46 bp    DNA             PAT       03-APR-1998
DEFINITION  Sequence 10 from patent US 5681697.
ACCESSION   I70986
VERSION     I70986.1  GI:3007121
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 46)
  AUTHORS   Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.
  TITLE     Solution phase nucleic acid sandwich assays having reduced
            background noise and kits therefor
  JOURNAL   Patent: US 5681697-A 10 28-OCT-1997;
FEATURES             Location/Qualifiers
     source          1. .46
                     /organism="unknown"
BASE COUNT        9 a     17 c      11 g      9 t
ORIGIN
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  Query Match             100.0%;  Score 20;  DB 10;  Length 46;
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  Matches   16;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 UUCGCGACCCAACACUACUC 20
           ::|||||||||||||||:||:|
Db      10 TTCGCGACCCAACACTACTC 29
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RESULT   8
AF282631/c
LOCUS       AF282631       139 bp    RNA             VRL       01-MAR-2001
DEFINITION  Hepatitis C virus isolate H069 clone I 5' non-coding region
            sequence.
ACCESSION   AF282631
VERSION     AF282631.1  GI:10764494
KEYWORDS    .
SOURCE      Hepatitis C virus.
  ORGANISM  Hepatitis C virus
            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
            Hepacivirus.
REFERENCE   1  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Diversity of Hepatitis C Virus Quasispecies Evaluated by Denaturing
            Gradient Gel Electrophoresis
  JOURNAL   Clin. Diagn. Lab. Immunol. 8 (1), 62-73 (2001)
   PUBMED   11139197
REFERENCE   2  (bases 1 to 139)
  AUTHORS   Harris,K.A. and Teo,C.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-JUN-2000) Hepatitis and Retrovirus Laboratory,
            Central Public Health Laboratory, 61 Colindale Avenue, London NW9
            5HT, UK
FEATURES             Location/Qualifiers
     source          1. .139
                     /organism="Hepatitis C virus"
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                     /db_xref="taxon:11103"
                     /clone="I"
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BASE COUNT       28 a     36 c      43 g      32 t
ORIGIN
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